

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=12; day=10; hr=10; min=32; sec=40; ms=917;
]

=====

Application No: 10550958 Version No: 1.0

Input Set:

Output Set:

Started: 2008-12-03 17:15:41.121
Finished: 2008-12-03 17:15:41.875
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 754 ms
Total Warnings: 3
Total Errors: 0
No. of SeqIDs Defined: 5
Actual SeqID Count: 5

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)

SEQUENCE LISTING

<110> Pohl, Jens
Bechtold, Rolf
Kruse, Michael

<120> Osteoinductive Materials

<130> 2923-725

<140> 10550958

<141> 2008-12-03

<150> PCT/EP04/003238

<151> 2004-03-26

<160> 5

<170> PatentIn version 3.5

<210> 1

<211> 2703

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (640)..(2142)

<220>

<221> misc_feature

<222> (2032)..(2034)

<223> n is a, c, g, or t

<400> 1

ccatggcctc gaaagggcag cgggtgatttt ttccacataa atatatcgca cttaaagtga 60

tttagacagc atgacatcag agagtaatta aattggtttg ggttgaatt ccgtttccaa 120

ttcttgagtt caggtttgta aaagattttt ctgagcacct gcaggcctgt gagtgtgtgt 180

gtgtgtgtgt gtgtgtgtgt gtgtgtgtga agtattttca ctggaaagga ttcaaaacta 240

gggggggaaa aaaaactgga gcacacaggc agcattacgc cattcttcct tcttgaaaa 300

tcctcagcc ttatacaagc ctcttcaag ccctcagtca gttgtgcagg agaaaggggg 360

cggttggctt tctcttttca agaacgagtt attttcagct gctgactgga gacggtgcac 420

gtctggatac gagagcattt ccactatggg actggataca aacacacacc cggcagactt 480

caagagtctc agactgagga gaaagccttt ccttctgctg ctactgctgc tgccgctgct 540

tttgaaagtc cactcctttc atggtttttc ctgccaacc agaggcacct ttgctgctgc 600

cgctgttctc tttggtgtca ttcagcggct ggccagagg atg aga ctc ccc aaa	654
Met Arg Leu Pro Lys	
1 5	
ctc ctc act ttc ttg ctt tgg tac ctg gct tgg ctg gac ctg gaa ttc	702
Leu Leu Thr Phe Leu Leu Trp Tyr Leu Ala Trp Leu Asp Leu Glu Phe	
10 15 20	
atc tgc act gtg ttg ggt gcc cct gac ttg ggc cag aga ccc cag ggg	750
Ile Cys Thr Val Leu Gly Ala Pro Asp Leu Gly Gln Arg Pro Gln Gly	
25 30 35	
acc agg cca gga ttg gcc aaa gca gag gcc aag gag agg ccc ccc ctg	798
Thr Arg Pro Gly Leu Ala Lys Ala Glu Ala Lys Glu Arg Pro Pro Leu	
40 45 50	
gcc cgg aac gtc ttc agg cca ggg ggt cac agc tat ggt ggg ggg gcc	846
Ala Arg Asn Val Phe Arg Pro Gly Gly His Ser Tyr Gly Gly Gly Ala	
55 60 65	
acc aat gcc aat gcc agg gca aag gga ggc acc ggg cag aca gga ggc	894
Thr Asn Ala Asn Ala Arg Ala Lys Gly Gly Thr Gly Gln Thr Gly Gly	
70 75 80 85	
ctg aca cag ccc aag aag gat gaa ccc aaa aag ctg ccc ccc aga ccg	942
Leu Thr Gln Pro Lys Lys Asp Glu Pro Lys Lys Leu Pro Pro Arg Pro	
90 95 100	
ggc ggc cct gaa ccc aag cca gga cac cct ccc caa aca agg cag gct	990
Gly Gly Pro Glu Pro Lys Pro Gly His Pro Pro Gln Thr Arg Gln Ala	
105 110 115	
aca gcc cgg act gtg acc cca aaa gga cag ctt ccc gga ggc aag gca	1038
Thr Ala Arg Thr Val Thr Pro Lys Gly Gln Leu Pro Gly Gly Lys Ala	
120 125 130	
ccc cca aaa gca gga tct gtc ccc agc tcc ttc ctg ctg aag aag gcc	1086
Pro Pro Lys Ala Gly Ser Val Pro Ser Ser Phe Leu Leu Lys Lys Ala	
135 140 145	
agg gag ccc ggg ccc cca cga gag ccc aag gag ccg ttt cgc cca ccc	1134
Arg Glu Pro Gly Pro Pro Arg Glu Pro Lys Glu Pro Phe Arg Pro Pro	
150 155 160 165	
ccc atc aca ccc cac gag tac atg ctc tcg ctg tac agg acg ctg tcc	1182
Pro Ile Thr Pro His Glu Tyr Met Leu Ser Leu Tyr Arg Thr Leu Ser	
170 175 180	
gat gct gac aga aag gga ggc aac agc agc gtg aag ttg gag gct ggc	1230
Asp Ala Asp Arg Lys Gly Gly Asn Ser Ser Val Lys Leu Glu Ala Gly	
185 190 195	
ctg gcc aac acc atc acc agc ttt att gac aaa ggg caa gat gac cga	1278
Leu Ala Asn Thr Ile Thr Ser Phe Ile Asp Lys Gly Gln Asp Asp Arg	
200 205 210	
ggg ccc gtg gtc agg aag cag agg tac gtg ttt gac att agt gcc ctg	1326

Gly	Pro	Val	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe	Asp	Ile	Ser	Ala	Leu	
215						220					225					
gag aag gat ggg ctg ctg ggg gcc gag ctg cgg atc ttg cgg aag aag																1374
Glu	Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg	Ile	Leu	Arg	Lys	Lys	
230					235				240						245	
ccc tcg gac acg gcc aag cca gcg gcc ccc gga ggc ggg cgg gct gcc																1422
Pro	Ser	Asp	Thr	Ala	Lys	Pro	Ala	Ala	Pro	Gly	Gly	Gly	Arg	Ala	Ala	
				250					255					260		
cag ctg aag ctg tcc agc tgc ccc agc ggc cgg cag ccg gcc tcc ttg																1470
Gln	Leu	Lys	Leu	Ser	Ser	Cys	Pro	Ser	Gly	Arg	Gln	Pro	Ala	Ser	Leu	
			265					270					275			
ctg gat gtg cgc tcc gtg cca ggc ctg gac gga tct ggc tgg gag gtg																1518
Leu	Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly	Ser	Gly	Trp	Glu	Val	
		280					285					290				
ttc gac atc tgg aag ctc ttc cga aac ttt aag aac tcg gcc cag ctg																1566
Phe	Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys	Asn	Ser	Ala	Gln	Leu	
	295					300					305					
tgc ctg gag ctg gag gcc tgg gaa cgg ggc agg gcc gtg gac ctc cgt																1614
Cys	Leu	Glu	Leu	Glu	Ala	Trp	Glu	Arg	Gly	Arg	Ala	Val	Asp	Leu	Arg	
310					315				320					325		
ggc ctg ggc ttc gac cgc gcc gcc cgg cag gtc cac gag aag gcc ctg																1662
Gly	Leu	Gly	Phe	Asp	Arg	Ala	Ala	Arg	Gln	Val	His	Glu	Lys	Ala	Leu	
				330					335					340		
ttc ctg gtg ttt ggc cgc acc aag aaa cgg gac ctg ttc ttt aat gag																1710
Phe	Leu	Val	Phe	Gly	Arg	Thr	Lys	Lys	Arg	Asp	Leu	Phe	Phe	Asn	Glu	
			345					350					355			
att aag gcc cgc tct ggc cag gac gat aag acc gtg tat gag tac ctg																1758
Ile	Lys	Ala	Arg	Ser	Gly	Gln	Asp	Asp	Lys	Thr	Val	Tyr	Glu	Tyr	Leu	
		360					365					370				
ttc agc cag cgg cga aaa cgg cgg gcc cca ctg gcc act cgc cag ggc																1806
Phe	Ser	Gln	Arg	Arg	Lys	Arg	Arg	Ala	Pro	Leu	Ala	Thr	Arg	Gln	Gly	
	375					380					385					
aag cga ccc agc aag aac ctt aag gct cgc tgc agt cgg aag gca ctg																1854
Lys	Arg	Pro	Ser	Lys	Asn	Leu	Lys	Ala	Arg	Cys	Ser	Arg	Lys	Ala	Leu	
390					395				400					405		
cat gtc aac ttc aag gac atg ggc tgg gac gac tgg atc atc gca ccc																1902
His	Val	Asn	Phe	Lys	Asp	Met	Gly	Trp	Asp	Asp	Trp	Ile	Ile	Ala	Pro	
			410					415					420			
ctt gag tac gag gct ttc cac tgc gag ggg ctg tgc gag ttc cca ttg																1950
Leu	Glu	Tyr	Glu	Ala	Phe	His	Cys	Glu	Gly	Leu	Cys	Glu	Phe	Pro	Leu	
			425					430					435			
cgc tcc cac ctg gag ccc acg aat cat gca gtc atc cag acc ctg atg																1998
Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	Val	Ile	Gln	Thr	Leu	Met	

440

445

450

aac tcc atg gac ccc gag tcc aca cca ccc acc nnn tgt gtg ccc acg 2046
 Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Xaa Cys Val Pro Thr
 455 460 465

cgg ctg agt ccc atc agc atc ctc ttc att gac tct gcc aac aac gtg 2094
 Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp Ser Ala Asn Asn Val
 470 475 480 485

gtg tat aag cag tat gag gac atg gtc gtg gag tcg tgt ggc tgc agg 2142
 Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg
 490 495 500

tagcagcact ggccctctgt cttcctgggt ggcacatccc aagagcccct tctgcactc 2202

ctggaatcac agaggggtca ggaagctgtg gcaggagcat ctacacagct tgggtgaaag 2262

gggattccaa taagcttgct cgctctctga gtgtgacttg ggctaaaggc ccccttttat 2322

ccacaagttc ccttggtgta ggattgctgc ccgtctgctg atgtgaccag tggcaggcac 2382

aggtccaggg agacagactc tgaatgggac tgagtcccag gaaacagtgc tttccgatga 2442

gactcagccc accattttctc ctcacctggg ccttctcage ctctggactc tectaagcac 2502

ctctcaggag agccacaggt gccactgcct cctcaaatca catttgtgcc tgggtgacttc 2562

ctgtccctgg gacagttgag aagctgactg ggcaagagtg ggagagaaga ggagagggct 2622

tggatagagt tgaggagtgt gaggctgtta gactgttaga tttaaagtga tattgatgag 2682

ataaaaagca aaactgtgcc t 2703

<210> 2

<211> 501

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (465)..(465)

<223> The 'Xaa' at location 465 stands for Lys, Asn, Arg, Ser, Thr,
 Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
 Cys, or Phe.

<400> 2

Met Arg Leu Pro Lys Leu Leu Thr Phe Leu Leu Trp Tyr Leu Ala Trp
 1 5 10 15

Leu Asp Leu Glu Phe Ile Cys Thr Val Leu Gly Ala Pro Asp Leu Gly
 20 25 30

Gln Arg Pro Gln Gly Thr Arg Pro Gly Leu Ala Lys Ala Glu Ala Lys
35 40 45

Glu Arg Pro Pro Leu Ala Arg Asn Val Phe Arg Pro Gly Gly His Ser
50 55 60

Tyr Gly Gly Gly Ala Thr Asn Ala Asn Ala Arg Ala Lys Gly Gly Thr
65 70 75 80

Gly Gln Thr Gly Gly Leu Thr Gln Pro Lys Lys Asp Glu Pro Lys Lys
85 90 95

Leu Pro Pro Arg Pro Gly Gly Pro Glu Pro Lys Pro Gly His Pro Pro
100 105 110

Gln Thr Arg Gln Ala Thr Ala Arg Thr Val Thr Pro Lys Gly Gln Leu
115 120 125

Pro Gly Gly Lys Ala Pro Pro Lys Ala Gly Ser Val Pro Ser Ser Phe
130 135 140

Leu Leu Lys Lys Ala Arg Glu Pro Gly Pro Pro Arg Glu Pro Lys Glu
145 150 155 160

Pro Phe Arg Pro Pro Pro Ile Thr Pro His Glu Tyr Met Leu Ser Leu
165 170 175

Tyr Arg Thr Leu Ser Asp Ala Asp Arg Lys Gly Gly Asn Ser Ser Val
180 185 190

Lys Leu Glu Ala Gly Leu Ala Asn Thr Ile Thr Ser Phe Ile Asp Lys
195 200 205

Gly Gln Asp Asp Arg Gly Pro Val Val Arg Lys Gln Arg Tyr Val Phe
210 215 220

Asp Ile Ser Ala Leu Glu Lys Asp Gly Leu Leu Gly Ala Glu Leu Arg
225 230 235 240

Ile Leu Arg Lys Lys Pro Ser Asp Thr Ala Lys Pro Ala Ala Pro Gly
245 250 255

Gly Gly Arg Ala Ala Gln Leu Lys Leu Ser Ser Cys Pro Ser Gly Arg

260

265

270

Gln Pro Ala Ser Leu Leu Asp Val Arg Ser Val Pro Gly Leu Asp Gly
 275 280 285

Ser Gly Trp Glu Val Phe Asp Ile Trp Lys Leu Phe Arg Asn Phe Lys
 290 295 300

Asn Ser Ala Gln Leu Cys Leu Glu Leu Glu Ala Trp Glu Arg Gly Arg
 305 310 315 320

Ala Val Asp Leu Arg Gly Leu Gly Phe Asp Arg Ala Ala Arg Gln Val
 325 330 335

His Glu Lys Ala Leu Phe Leu Val Phe Gly Arg Thr Lys Lys Arg Asp
 340 345 350

Leu Phe Phe Asn Glu Ile Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr
 355 360 365

Val Tyr Glu Tyr Leu Phe Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu
 370 375 380

Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys
 385 390 395 400

Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp Asp Asp
 405 410 415

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Leu
 420 425 430

Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val
 435 440 445

Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr
 450 455 460

Xaa Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp
 465 470 475 480

Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu
 485 490 495

Ser Cys Gly Cys Arg
500

<210> 3
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> REPEAT
<222> (3)..(3)
<223> Xaa=(Y)25-29 with Y=any amino acid including cysteine

<220>
<221> VARIANT
<222> (5)..(7)
<223> Xaa=Y with Y=any amino acid including cysteine

<220>
<221> REPEAT
<222> (9)..(9)
<223> Xaa=X with X=any amino acid except cysteine

<220>
<221> VARIANT
<222> (10)..(10)
<223> Xaa=X with X=any amino acid except cysteine

<220>
<221> REPEAT
<222> (12)..(12)
<223> Xaa=(Y)27-34 with Y=any amino acid including cysteine

<220>
<221> VARIANT
<222> (14)..(14)
<223> Xaa=Y with Y=any amino acid including cysteine

<400> 3

Cys Cys Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Cys
1 5 10 15

<210> 4
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> consensus sequence

<220>

<221> REPEAT

<222> (2)..(2)

<223> Xaa=(Y)28 with Y=any amino acid including cysteine

<220>

<221> VARIANT

<222> (4)..(6)

<223> Xaa=Y wtih Y=any amino acid including cysteine

<220>

<221> REPEAT

<222> (8)..(8)

<223> Xaa=(Y)30-32 with Y=any amino acid including cysteine

<220>

<221> VARIANT

<222> (9)..(9)

<223> Xaa=X with X=any amino acid except cysteine

<220>

<221> REPEAT

<222> (11)..(11)

<223> Xaa=(Y)31 with Y=any amino acid including cysteine

<220>

<221> VARIANT

<222> (13)..(13)

<223> Xaa=Y with Y=any amino acid including cysteine

<400> 4

Cys Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Cys

1 5 10

<210> 5

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<220>

<221> REPEAT

<222> (2)..(2)

<223> Xaa=(X)28 with X=any amino acid except cysteine

<220>

<221> VARIANT

<222> (4)..(6)

<223> Xaa=X with X=any amino acid except cysteine

<220>
<221> REPEAT
<222> (8)..(8)
<223> Xaa=(X)31-33 with X=any amino acid except cysteine

<220>
<221> REPEAT
<222> (10)..(10)
<223> Xaa=(X)31 with X=any amino acid except cysteine

<220>
<221> VARIANT
<222> (12)..(12)
<223> Xaa=X with X=any amino acid except cysteine

<400> 5

Cys Xaa Cys Xaa Xaa Xaa Cys Xaa Cys Xaa Cys Xaa Cys
1 5 10